SEQUENCE LISTING

<110> Falco, Saverio Carl
Famodu, Layo
Rafalski, Jan A.
Ramaker, Michael
Tarczynski, Mitchell C.
Thorpe, Catherine

<120> PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE METHIONINE CONTENT OF THE SEEDS OF PLANTS

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<151> August 27, 1996

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35 40 45

Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Ser Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Glu
65 70 75 80

Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly Leu Ser Thr Tyr Phe Ser
85 90 95

Met Ala Arg Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
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Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Ser Thr
115 120 125

Lys Phe Thr Tyr Ala Ser His Lys Ala Val Ser Glu Tyr Lys Glu Ala
130 135 140

Lys Ala Leu Gly Ile Asp Thr Val Pro Val Leu Val Gly Pro Val Ser
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Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
165 170 175

Leu Leu Ser Leu Leu Gly Ser Ile Leu Pro Ile Tyr Lys Glu Val Val
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Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Leu Asp Glu Pro
195 200 205

Thr Leu Val Lys Asp Leu Asp Ala His Glu Leu Ala Ala Phe Ser Ser
210 215 220

Ala Tyr Ala Glu Leu Glu Ser Ser Phe Ser Gly Leu Asn Val Leu Ile
225 230 235 240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ser Tyr Lys Thr Leu Thr
245 250 255

Ser Leu Ser Gly Val Thr Ala Tyr Gly Phe Asp Leu Ile Arg Gly Ala
260 265 270

Lys Thr Leu Asp Leu Ile Arg Ser Ser Phe Pro Ser Gly Lys Tyr Leu
275 280 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asp Asp Leu Ala
290 295 300

Ala Ser Leu Ser Thr Leu His Ser Leu Glu Ala Val Ala Gly Lys Asp
305 310 315 320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Met His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ala Gly Gln Lys Asp Glu Val Tyr Phe Ala Ala Asn Ala Ala Ala Gln
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Ala Ser Arg Arg Ser Ser Pro Arg Val Thr Asn Glu Glu Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ser Thr Thr Val
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Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Thr Glu Asp Glu Tyr Ile
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Ser Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Ile Gln Glu Glu
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Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
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Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
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Met Ala Gln Ser Met Thr Pro Arg Pro Met Lys Gly Met Leu Thr Gly
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Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
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Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Lys Glu Val Glu
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Asp Leu Glu Ala Ala Gly Ile Gln Val Ile Gln Ile Asp Glu Ala Ala
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Leu Arg Glu Gly Leu Pro Leu Arg Lys Ser Glu His Ala Phe Tyr Leu
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Asp Trp Ala Val His Ser Phe Arg Ile Thr Asn Cys Gly Val Gln Asp
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Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
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Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
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Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
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Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Glu Lys Met Leu Ala
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Val Phe Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
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35 40 45

Met Ala Gly Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Phe
50 55 60

Tyr Asp Gln Leu Leu Asp Ala Thr Ala Thr Leu Gly Ala Val Pro Pro
65 70 75 80

Arg Tyr Gly Trp Thr Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
85 90 95

Met Ala Arg Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
100 105 110

Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
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Asn Phe Thr Xaa Ala Ser Gln Lys Ala Val Asp Glu Tyr Lys Glu Ala
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Lys Ala Leu Gly Val Asp Thr Ile Pro Val Leu Val Gly Pro Val Thr
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Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
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Leu Leu Ser Leu Leu Pro Lys Val Leu Ala Val Tyr Lys Glu Val Ile
            180   185   190

Ala Asp Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
        195   200   205

Thr Leu Val Leu Asp Leu Glu Ser His Lys Leu Gln Ala Phe Thr Asp
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Ala Tyr Ala Glu Leu Ala Pro Ala Leu Ser Asp Leu Asn Val Leu Val
225   230   235   240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ala Tyr Lys Thr Leu Thr
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Ser Leu Asn Gly Val Thr Ala Tyr Gly Phe Asp Leu Val Arg Gly Thr
            260   265   270

His Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
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Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
    290   295   300

Ala Ser Leu Thr Thr Leu Gln Gly Leu Glu Gly Ile Val Gly Lys Asp
305   310   315   320

Lys Leu Val Val Ser Thr Ser Ser Ser Leu Leu His Thr Ala Val Asp
                325   330   335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
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Phe Ala Ala Gln Lys Ile Val Glu Val Asn Ala Leu Ala Lys Ala Leu
        355   360   365

Ser Gly Asn Lys Asp Val Ala Phe Phe Ser Ala Asn Ala Ala Ala Gln
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Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
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Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
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Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Ile Leu
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Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
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Val Arg Arg Glu Phe Lys Ala Asn Lys Ile Ser Glu Glu Glu Tyr Val
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Lys Ser Ile Lys Glu Glu Ile Arg Lys Val Val Glu Leu Gln Glu Glu
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Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
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Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Val Asn
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Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
515 520 525

Tyr Gly Asp Val Ser Arg Pro Lys Pro Met Thr Val Phe Trp Ser Ser
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Leu Ala Gln Ser Phe Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
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Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Ser Glu Thr Thr Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
580 585 590

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ser Glu Gln Ala His Tyr Leu
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Asp Trp Ala Val His Ala Phe Arg Ile Thr Asn Val Gly Val Gln Asp
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Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
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Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
660 665 670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Pro Thr Glu Glu Ile Ala Asp Arg Ile Asn Lys Met Leu Ala
705 710 715 720

Val Leu Glu Lys Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
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Ala Ala Lys Leu Ile Arg Tyr Glu Leu Ala Lys
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Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Ala
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Arg Tyr Asn Trp Ala Gly Gly Glu Ile Ala Phe Asp Thr Tyr Phe Ser
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Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
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Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
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Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asp Glu Tyr Lys Glu Ala
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Lys Gly Leu Gly Val Asp Thr Val Pro Val Leu Ile Gly Pro Val Ser
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Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Pro
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Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
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Thr Leu Val Leu Asp Leu Gln Ala His Gln Leu Glu Ala Phe Thr Lys
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Ala Tyr Ala Glu Leu Glu Ser Ser Leu Ser Gly Leu Asn Val Leu Thr
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Glu Thr Tyr Phe Ala Asp Val Pro Ala Glu Ala Phe Lys Thr Leu Thr
245 250 255

Ala Leu Lys Gly Val Thr Ala Phe Gly Phe Asp Leu Val Arg Gly Ala
260 265 270

Gln Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
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Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
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Ala Ser Leu Asn Leu Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
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Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ala Gly His Lys Asp Glu Ala Phe Phe Ser Ala Asn Ala Thr Ala Gln
370 375 380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
405 410 415

Ser Ser Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Glu Glu Tyr Val
450 455 460

Lys Ala Ile Lys Ala Glu Ile Lys Lys Val Val Asp Leu Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
500 505 510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
515 520 525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
530 535 540

Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545 550 555 560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
580 585 590

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
610 615 620

Asn Trp Ala Val His Ser Phe Arg Ile Thr Asn Val Gly Ile Gln Asp
625 630 635 640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
645 650 655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
660 665 670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Asn Lys Met Leu Ala
705 710 715 720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
725 730 735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
740 745 750

Ala Ala Lys Ala Ile Arg Thr Gln Leu Ala Ser Ser Lys
755 760 765

<210> 7
<211> 475
<212> DNA
<213> Triticum aestivum

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agctcaagtt tgccttggag tctttctggg atgggaagag cagcgctgag gatttggaga 180
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gtgccgtccc ggaccgctac tcatggactg gcggagagat tggncacagc acctacttct 360
caatggncaa gggcaatgcc actgtccctg ctatggagat gaccaagtgg tttgacacca 420
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<210> 8
<211> 124
<212> PRT
<213> Triticum aestivum

<220>
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<222> (98)

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<221> UNSURE
<222> (120)

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Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
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Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
20 25 30

Asp Leu Glu Lys Val Ala Ala Asp Leu Arg Ala Ser Ile Trp Lys Gln
35 40 45

Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Asp
65 70 75 80

Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly His Ser Thr Tyr Phe Ser
85 90 95

Met Xaa Lys Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
100 105 110

Phe Asp Thr Asn Xaa His Phe Xaa Val Pro Glu Leu
115 120

<210> 9
<211> 628
<212> DNA
<213> Triticum aestivum

<220>
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<222> (219)

<220>
<221> unsure
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<400> 9
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accttcctat cctcccaaca acaacaattg gttcattccc tcagacaatg gacctcagga 180
gggtccgccg tgagtacaag gcgaaagaag atctctgang aggagtatgt cagtgctatc 240
aaggaagaaa ttancaaagg ttgtcaagat tcaaagagga gcttgacatt gatgttctcn 300
tccaatggag aagcctgana aaaatgacat nggtnaanta cttcggcnan caaattatcn 360
gggtttgcaa ttactgccaa tggatgggtg caatcctatg gattacttgc gtnaancacc 420
gatnatcnat gggatgtaan cgcccaaccc atganatctt ctggtcaana tgntcaggac 480
atancctccc ccaatgaagg aatntnacgg cctttaaatc ccaacnggct ttntnagaac 540
acaaccaggt tnagaatgca caaattcnct gccataaaan gagttaggtt ccagctgngn 600
atcagngtca atnatagggg ccaaaagg 628

<210> 10
<211> 118
<212> PRT
<213> Triticum aestivum

<220>
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<222> (8)

<220>
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<222> (72)..(73)

<220>
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<222> (116)

<400> 10
Ser Ser Pro Arg Val Asn Asn Xaa Glu Val Gln Lys Ala Ala Ala Ala
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Leu Lys Gly Ser Asp His Arg Arg Ala Thr Pro Val Ser Ala Arg Leu
20 25 30

Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Ile Leu Pro Thr Thr Thr
35 40 45

Ile Gly Ser Phe Pro Gln Thr Met Asp Leu Arg Arg Val Arg Arg Glu
50 55 60

Tyr Lys Ala Lys Glu Asp Leu Xaa Xaa Gly Val Cys Gln Cys Tyr Gln
65 70 75 80

Gly Arg Asn Xaa Gln Arg Leu Ser Arg Phe Lys Glu Glu Leu Asp Ile
85 90 95

Asp Val Leu Xaa Gln Trp Arg Ser Leu Xaa Lys Met Thr Xaa Val Xaa
100 105 110

Tyr Phe Gly Xaa Gln Ile
115

<210> 11
<211> 765
<212> PRT
<213> Catharanthus roseus

<400> 11
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
1 5 10 15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Lys Lys Ser Ser Ala Glu
20 25 30

Asp Leu Gln Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
35 40 45

Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Ala Thr Met Leu Gly Ala Val Pro Pro
65 70 75 80

Arg Tyr Asn Phe Ala Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
85 90 95

Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
100 105 110

Phe Asp Thr Asn Tyr His Tyr Ile Val Pro Glu Leu Gly Pro Glu Val
115 120 125

Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asn Glu Tyr Lys Glu Ala
130 135 140

Lys Glu Leu Gly Val Asp Thr Val Pro Val Leu Val Gly Pro Val Thr
145 150 155 160

Phe Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Thr Phe Pro
165 170 175

Leu Leu Ser Leu Leu Asp Lys Ile Leu Pro Val Tyr Lys Glu Val Ile
180 185 190

Gly Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
195 200 205

Thr Leu Val Leu Asp Leu Glu Ser His Gln Leu Glu Ala Phe Thr Lys
210 215 220

Ala Tyr Ser Glu Leu Glu Ser Thr Leu Ser Gly Leu Asn Val Ile Val
225 230 235 240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Thr Tyr Lys Ile Leu Thr
245 250 255

Ala Leu Lys Gly Val Thr Gly Phe Gly Phe Asp Leu Val Arg Gly Ala
260 265 270

Lys Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
275 280 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
290 295 300

Ala Ser Leu Ser Thr Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
305 310 315 320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Pro Lys Leu Asp Lys Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ala Gly Glu Lys Asp Glu Ala Phe Phe Ser Glu Asn Ala Ala Ala Gln
370 375 380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Gln Ala Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ala Thr Thr Val
405 410 415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Leu Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Asp Asp Tyr Val
450 455 460

Lys Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Leu Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
500 505 510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
515 520 525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Gln
530 535 540

Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545 550 555 560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
580 585 590

Asp Leu Glu Lys Ala Gly Ile Asn Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
610 615 620

Asp Trp Ala Val His Ser Phe Arg Ile Thr Asn Leu Pro Leu Gln Asp
625 630 635 640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
645 650 655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Met Thr Ile Glu Asn
660 665 670

Ser Arg Ser Ser Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Ile Asn Lys Met Leu Ala
705 710 715 720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
725 730 735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
740 745 750

Ala Ala Lys Leu Ile Arg Thr Gln Leu Ala Ser Ala Lys
755 760 765

<210> 12
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12
atccaacaat gtgagatgtc atgaattctg ac 32

<210> 13
<211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13
gtcagaattc atgacatctc acattgttgg at 32

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
ctcacggtcc gatgagaagc tcct 24

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15
gatcggtacc tcacttggag ctggcaagtt g 31

<210> 16
<211> 1638
<212> DNA
<213> Zea mays

<400> 16
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cgaaacccta gctcctctta cgccatggcc accgtgtcgc tcactccgca ggcggtcttc 120
tccaccgagt ccggcggcgc cctggcctct gccaccatcc tccgcttccc gccaaacttc 180
gtccgcctcc gcggcggcgg atgtcagcgc aattcctaac gctaaggttg cgcagccgtc 240
cgccgtcgta ttggccgagc gtaacctgct cggctccgac gccagcctcg ccgtccacgc 300
gggggagagg ctgggaagaa ggatagccac ggatgctatc accacgccgg tagtgaacac 360
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tagcttcgag tatgggaggt atgggaaccc gaccacggag gcattagaga agaagatgag 480
cgcactggag aaagcagagt ccaccgtgtt tgtggcgtca gggatgtatg cagctgtggc 540
tatgctcagc gcacttgtcc ctgctggtgg gcacattgtg accaccacgg attgctaccg 600
caagacaagg atttacatgg aaaatgagct ccctaagagg ggaatttcga tgactgtcat 660
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tcaagatctg tgacaatgat atgagctgat gactgcgaat aagttctctt ttgcttattt 1560

tatccgtcaa attcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaaa aactcgag 1638

<210> 17
<211> 480
<212> PRT
<213> Zea mays

<400> 17

Asn Ser Gly Ser Lys Pro Pro Arg Pro Asn Glu Arg Ser Val Pro Ser
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Arg Ala Asp Ala Glu Thr Leu Ala Pro Leu Thr Pro Trp Pro Pro Cys
20 25 30

Arg Ser Leu Arg Arg Arg Ser Ser Pro Pro Ser Pro Ala Ala Pro Trp
35 40 45

Pro Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser Ser Ala Ser Ala
50 55 60

Ala Ala Asp Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser
65 70 75 80

Ala Val Val Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu
85 90 95

Ala Val His Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala
100 105 110

Ile Thr Thr Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser
115 120 125

Gln Glu Leu Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr
130 135 140

Gly Arg Tyr Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser
145 150 155 160

Ala Leu Glu Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr
165 170 175

Ala Ala Val Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile
180 185 190

Val Thr Thr Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn
195 200 205

Glu Leu Pro Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp
210 215 220

Met Asp Ala Leu Gln Asn Ala Leu Asp Asn Asn Asn Val Ser Leu Phe
225 230 235 240

Phe Thr Glu Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu
245 250 255

His Val Ser Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp
260 265 270

Ser Thr Phe Ala Ser Pro Ile Asn Gln Lys Ala Leu Thr Leu Gly Ala
275 280 285

Asp Leu Val Ile His Ser Ala Thr Lys Tyr Ile Ala Gly His Asn Asp
290 295 300

Val Ile Gly Gly Cys Val Ser Gly Arg Asp Glu Leu Val Ser Lys Val
305 310 315 320

Arg Ile Tyr His His Val Val Gly Gly Val Leu Asn Pro Asn Ala Ala
325 330 335

Tyr Leu Ile Leu Arg Gly Met Lys Thr Leu His Leu Arg Val Gln Cys
340 345 350

Gln Asn Asp Thr Ala Leu Arg Met Ala Gln Phe Leu Glu Glu His Pro
355 360 365

Lys Ile Ala Arg Val Tyr Tyr Pro Gly Leu Pro Ser His Pro Glu His
370 375 380

His Ile Ala Lys Ser Gln Met Thr Gly Phe Gly Gly Val Val Ser Phe
385 390 395 400

Glu Val Ala Gly Asp Phe Asp Ala Thr Arg Lys Phe Ile Asp Ser Val
405 410 415

Lys Ile Pro Tyr His Ala Pro Ser Phe Gly Gly Cys Glu Ser Ile Ile
420 425 430

Asp Gln Pro Ala Ile Met Ser Tyr Trp Asp Ser Lys Glu Gln Arg Asp
435 440 445

Ile Tyr Gly Ile Lys Asp Asn Leu Ile Arg Phe Ser Ile Gly Val Glu
450 455 460

Asp Phe Glu Asp Leu Lys Asn Asp Leu Val Gln Ala Leu Glu Lys Ile
465 470 475 480

<210> 18
<211> 3639
<212> DNA
<213> Zea mays

<400> 18
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ttatcaccat gtggttggtg gtgttctaaa cccggtaagt ttagattgtt aaagttttgt 3060
ttccatttat ttcatcttcc ttgcacaggt tgtatgtatt tacagattcc catagttaca 3120
agcttctatt tttataggta gaaaatcgtg taattttctt tagtagcata tgtttaggtt 3180
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tttcaaatca tgactaggat tctagttgcc cggacaccga ctaggtgatt aatcgtgact 3480
aggcattgac tagtcacgat tagttttgag ctagtcgaac ttatcaacaa cttgttccag 3540
gcaatatatt gcagtactat gccttattga ttgggtatat aaatgaattt tagcacacag 3600
atagagcaga agtaagacaa attaacacaa agttctaga 3639

<210> 19
<211> 509
<212> PRT
<213> Zea mays

<400> 19
Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser
1 5 10 15

Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe
20 25 30

Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly
35 40 45

Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Pro Ala Ala Arg
50 55 60

Pro His Leu Gly Gly Gly Gly Arg Arg Ala Arg Gly Val Ala Ser Ser
65 70 75 80

His Ala Ala Ala Ala Ser Ala Ala Ala Ala Ala Ser Ala Ala Ala Glu
85 90 95

Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser Ala Val Val
100 105 110

Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu Ala Val His
115 120 125

Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala Ile Thr Thr
130 135 140

Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser Gln Glu Leu
145 150 155 160

Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr Gly Arg Tyr
165 170 175

Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser Ala Leu Glu
180 185 190

Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr Ala Ala Val
195 200 205

Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile Val Thr Thr
210 215 220

Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn Glu Leu Pro
225 230 235 240

Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp Met Asp Ala
245 250 255

Leu Gln Asn Ala Leu Asp Asn Asn Asn Val Ser Leu Phe Phe Thr Glu
260 265 270

Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu His Val Ser
275 280 285

Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp Ser Thr Phe
290 295 300

Ala Ser Pro Ile Asn Gln Lys Ala Leu Thr Leu Gly Ala Asp Leu Val
305 310 315 320

Ile His Ser Ala Thr Lys Tyr Ile Ala Gly His Asn Asp Val Ile Gly
325 330 335

Gly Cys Val Ser Gly Arg Asp Glu Leu Val Ser Lys Val Arg Ile Tyr
340 345 350

His His Val Val Gly Gly Val Leu Asn Pro Asn Ala Ala Tyr Leu Ile
355 360 365

Leu Arg Gly Met Lys Thr Leu His Leu Arg Val Gln Cys Gln Asn Asp
370 375 380

Thr Ala Leu Arg Met Ala Gln Phe Leu Glu Glu His Pro Lys Ile Ala
385 390 395 400

Arg Val Tyr Tyr Pro Gly Leu Pro Ser His Pro Glu His His Ile Ala
405 410 415

Lys Ser Gln Met Thr Gly Phe Gly Gly Val Val Ser Phe Glu Val Ala
420 425 430

Gly Asp Phe Asp Ala Thr Arg Lys Phe Ile Asp Ser Val Lys Ile Pro
435 440 445

Tyr His Ala Pro Ser Phe Gly Gly Cys Glu Ser Ile Ile Asp Gln Pro
450 455 460

Ala Ile Met Ser Tyr Trp Asp Ser Lys Glu Gln Arg Asp Ile Tyr Gly
465 470 475 480

Ile Lys Asp Asn Leu Ile Arg Phe Ser Ile Gly Val Glu Asp Phe Glu
485 490 495

Asp Leu Lys Asn Asp Leu Val Gln Ala Leu Glu Lys Ile
500 505

<210> 20
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20 14
aattcatgag tgca

<210> 21
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21 14
aatttgcact catg

<210> 22
<211> 1350
<212> DNA
<213> Escherichia coli

<400> 22
atggctgaaa ttgttgtctc caaatttggc ggtaccagcg tagctgattt tgacgccatg 60
aaccgcagcg ctgatattgt gctttctgat gccaacgtgc gtttagttgt cctctcggct 120
tctgctggta tcactaatct gctggtcgct ttagctgaag gactggaacc tggcgagcga 180
ttcgaaaaac tcgacgctat ccgcaacatc cagtttgcca ttctggaacg tctgcgttac 240
ccgaacgtta tccgtgaaga gattgaacgt ctgctggaga acattactgt tctggcagaa 300
gcggcggcgc tggcaacgtc tccggcgctg acagatgagc tggtcagcca cggcgagctg 360
atgtcgaccc tgctgtttgt tgagatcctg cgcgaacgcg atgttcaggc acagtggttt 420
gatgtacgta aagtgatgcg taccaacgac cgatttggtc gtgcagagcc agatatagcc 480
gcgctggcgg aactggccgc gctgcagctg ctcccacgtc tcaatgaagg cttagtgatc 540
acccagggat ttatcggtag cgaaaataaa ggtcgtacaa cgacgcttgg ccgtggaggc 600
agcgattata cggcagcctt gctggcggag gctttacacg catctcgtgt tgatatctgg 660
accgacgtcc cgggcatcta caccaccgat ccacgcgtag tttccgcagc aaaacgcatt 720
gatgaaatcg cgtttgccga agcggcagag atggcaactt ttggtgcaaa agtactgcat 780
ccggcaacgt tgctacccgc agtacgcagc gatatcccgg tctttgtcgg ctccagcaaa 840
gacccacgcg caggtggtac gctggtgtgc aataaaactg aaaatccgcc gctgttccgc 900
gctctggcgc ttcgtcgcaa tcagactctg ctcactttgc acagcctgaa tatgctgcat 960
tctcgcggtt tcctcgcgga agttttcggc atcctcgcgc ggcataatat ttcggtagac 1020
ttaatcacca cgtcagaagt gagcgtggca ttaacccttg ataccaccgg ttcaacctcc 1080
actggcgata cgttgctgac gcaatctctg ctgatggagc tttccgcact gtgtcgggtg 1140
gaggtggaag aaggtctggc gctggtcgcg ttgattggca atgacctgtc aaaagcctgc 1200
gccgttggca aagaggtatt cggcgtactg gaaccgttca acattcgcat gatttgttat 1260

ggcgcatcca gccataacct gtgcttcctg gtgcccggcg aagatgccga gcaggtggtg 1320
caaaaactgc atagtaattt gtttgagtaa 1350

<210> 23
<211> 449
<212> PRT
<213> Escherichia coli

<400> 23

Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp
1 5 10 15

Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
20 25 30

Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
35 40 45

Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
50 55 60

Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
65 70 75 80

Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
85 90 95

Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
100 105 110

Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
115 120 125

Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys
130 135 140

Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala
145 150 155 160

Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu
165 170 175

Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg
180 185 190

Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu
195 200 205

Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro
210 215 220

Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile
225 230 235 240

Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala
245 250 255

Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile
260 265 270

Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu
275 280 285

Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu
290 295 300

Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His
305 310 315 320

Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn
325 330 335

Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr
340 345 350

Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
355 360 365

Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
370 375 380

Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
385 390 395 400

Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
405 410 415

Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
420 425 430

Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
435 440 445

Glu

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
gatccatggc tgaaattgtt gtctccaaat ttggcg 36

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
gtaccgccaa atttggagac aacaatttca gccatg 36

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 26
atggcagcca agatgcttgc attgttcgct 30

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 27
gaatgcagca ccaacaaagg gttgctgtaa 30

<210> 28
<211> 2123
<212> DNA
<213> Zea mays

<400> 28
tctagagcct attaccatct ctactcacgg gtcgtagagg tggtgaggta ggctacagct 60
ggtgacaatc ctactcaccc tttgtaatcc tctacggctc tacgcgtagt taattggtta 120
gatgtcaacc ccctctctaa gtggcagtag tgggcttggt tatacctgct agtgcctggg 180
gatgttctat ttttctagta gtgcttgatc aaacattgca tagtttgact tgggacaaac 240
tgtctgatat atatatatat ttttgggcag agggagcagt aagaacttat ttagaaatgt 300
aatcatttgt taaaaaaggt ttaattttgc tgctttcttt cgttaatgtt gttttcacat 360
tagattttct ttgtgttata tacactggat acatacaaat tcagttgcag tagtctctta 420
atccacatca gctaggcata ctttagcaaa agcaaattac acaaatctag tgtgcctgtc 480
gtcacattct caataaactc gtcatgtttt actaaaagta ccttttcgaa gcatcatatt 540
aatccgaaaa cagttaggga agtctccaaa tctgaccaaa tgccaagtca tcgtccagct 600
tatcagcatc caactttcag tttcgcatgt gctagaaatt gtttttcatc tacatggcca 660
ttgttgactg catgcatcta taaataggac ctagacgatc aatcgcaatc gcatatccac 720
tattctctag gaagcaaggg aatcacatcg ccatggcagc caagatgttt gcattgtttg 780
cgctcctagc tctttgtgca accgccacta gtgctaccca tatcccaggg cacttgtcac 840
cactactgat gccattggct accatgaacc catggatgca gtactgcatg aagcaacagg 900
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caccaatgat gatgccgagc atggtgtcac caatgatgat gccaaacatg atgacagtgc 1260
cacaatgtta ctctggttct atctcacaca ttatacaaca acaacaatta ccattcatgt 1320
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cattctagat ctagatataa gcatttgtgt agtacccaat aatgaagtcg gcatgccatc 1440
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ttatatctct ccatgtctgt ttgtgtgttt gtaatgtctg ttaatcttag tagattatat 1560
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tagttttaac catacctaga cattatgtat atataggcgg cttaacaaaa gctatgtact 1680
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aggtgagtac ttgtgcgttg caacgggaac atataataac ataataactt atatacaaaa 1800
tgtatcttat attgttataa aaaatatttc ataatccatt tgtaatccta gtcatacata 1860
aattttgtta ttttaattta gttgtttcac tactacattg caaccattag tatcatgcag 1920
acttcgatat atgccaagat ttgcatggtc tcatcattga agagcacatg tcacacctgc 1980
cggtagaagt tctctcgtac attgtcagtc atcaggtacg caccaccata cacgcttgct 2040
taaacaaaaa aacaagtgta tgtgtttgcg aagagaatta agacaggcag acacaaagct 2100
acccgacgat ggcgagtcgg tca 2123

<210> 29
<211> 211
<212> PRT
<213> Zea mays

<400> 29
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
1 5 10 15

Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
20 25 30

Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
35 40 45

Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
50 55 60

Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
65 70 75 80

Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
85 90 95

Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
100 105 110

Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
115 120 125

Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
130 135 140

Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145 150 155 160

Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
165 170 175

Ile Ser His Ile Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
180 185 190

Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
195 200 205

Ala Ala Phe
210

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 30 17
atgaaccctt ggatgca

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 31 17
cccacagcaa tggcgat

<210> 32
<211> 639
<212> DNA
<213> Zea mays

<400> 32
ccatggcagc caagatgttt gcattgtttg cgctcctagc tctttgtgca accgccacta 60
gtgctaccca tatcccaggg cacttgtcac cactactgat gccattggct accatgaacc 120
cttggatgca gtactgcatg aagcaacagg gggttgccaa cttgttagcg tggccgaccc 180
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc 240
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg 300
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa 360
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga 420
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac 480
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca 540
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atcccaccca 600
tgttcttaca gcagcccttt gttggtgctg cattctaga 639

<210> 33
<211> 211
<212> PRT
<213> Zea mays

<400> 33
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
1 5 10 15

Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
20 25 30

Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
35 40 45

Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
50 55 60

Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
65 70 75 80

Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
85 90 95

Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
100 105 110

Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
115 120 125

Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
130 135 140

Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145 150 155 160

Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
165 170 175

Ile Ser His Ile Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
180 185 190

Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
195 200 205

Ala Ala Phe
210

<210> 34
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 34 13
ctagcccggg tac

<210> 35
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 35 13
ctaggtaccc ggg

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 36 30
ccacttcatg acccatatcc cagggcactt

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 37 30
ttctatctag aatgcagcac caacaaaggg

<210> 38
<211> 579
<212> DNA
<213> Zea mays

<400> 38
tcatgaccca tatcccaggg cacttgtcac cactactgat gccattggct accatgaacc 60
cttggatgca gtactgcatg aagcaacagg gggttgccaa cttgttagcg tggccgaccc 120
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc 180
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg 240
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa 300
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga 360
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac 420
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca 480
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atcccaccca 540
tgttcttaca gcagcccttt gttggtgctg cattctaga 579

<210> 39
<211> 191
<212> PRT
<213> Zea mays

<400> 39
Met Thr His Ile Pro Gly His Leu Ser Pro Leu Leu Met Pro Leu Ala
1 5 10 15

Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln Gln Gly Val Ala
20 25 30

Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln Leu Leu Ala Ser
35 40 45

Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro Gly Met Met Pro
50 55 60

Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro Ser Met Met Val
65 70 75 80

Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met Met Pro Pro Met
85 90 95

Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro Ser Met Met Pro
100 105 110

Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile Met Pro Ser Met
115 120 125

Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro Met Met Met Pro
130 135 140

Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser Ile Ser His Ile
145 150 155 160

Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro Thr Ala Met Ala
165 170 175

Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly Ala Ala Phe
180 185 190

<210> 40
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 40
ctagaagcct cggcaacgtc agcaacggcg gaagaatccg gtg 43

<210> 41
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 41
catgcaccgg attcttccgc cgttgctgac gttgccgagg ctt 43

<210> 42
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 42
gatcccatgg cgccccttaa gtccaccgcc agcctccccg tcgcccgccg ctcct 55

<210> 43
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 43
ctagaggagc ggcgggcgac ggggaggctg gcggtggact taaggggcgc catgg 55

<210> 44
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 44
catggcgccc accgtgatga tggcctcgtc ggccaccgcc gtcgctccgt tccaggggc 59

<210> 45
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 45
ttaagcccct ggaacggagc gacggcggtg gccgacgagg ccatcatcac ggtgggcgc 59

<210> 46
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 46
catggctggc ttccccacga ggaagaccaa caatgacatt acctccattg ctagcaacgg 60
tggaagagta caatg 75

<210> 47
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 47
catgcattgt actcttccac cgttgctagc aatggaggta atgtcattgt tggtcttcct 60
cgtggggaag ccagc 75

<210> 48
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 48
catggcttcc tcaatgatct cctccccagc tgttaccacc gtcaaccgtg ccggtgccgg 60
catggttgct ccattcaccg gcctcaaaag 90

<210> 49
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 49
catgcttttg aggccggtga atggagcaac catgccggca ccggcacggt tgacggtggt 60
aacagctggg gaggagatca ttgaggaagc 90

<210> 50
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 50
gactatccat ggcacattgt actcttccac c 31

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 51
tactaaccat ggcttcctca 20

<210> 52
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 52
ggccatggcc gc 12

<210> 53
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 53
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<210> 54
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 54
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<210> 55
<211> 1494
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1461)

<220>
<221> unsure
<222> (1464)

<220>
<221> unsure
<222> (1465)

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